OIPE

RAW SEQUENCE LISTING   DATE: 03/27/2002
PATENT APPLICATION: US/10/016,236   TIME: 10:39:22

Input Set : N:\Crf3\RULE60\10016236.raw
Output Set: N:\CRF3\03272002\J016236.raw

SEQUENCE LISTING
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 3  (1) GENERAL INFORMATION:
 5       (i) APPLICANT: Ryals, John
 6                      Friedrich, Leslie
 7                      Uknes, Scott
 8                      Molina, Antonio
 9                      Ruess, Wilhelm
10                      Knauf-Beiter, Gertrude
11                      Kung, Ruth
12                      Kessmann, Helmut
13                      Oostendorp, Michael
16      (ii) TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
18     (iii) NUMBER OF SEQUENCES: 32
20      (iv) CORRESPONDENCE ADDRESS:
21           (A) ADDRESSEE: Novartis Corporation
22           (B) STREET: 3054 Cornwallis Road
23           (C) CITY: Research Triangle Park
24           (D) STATE: North Carolina
25           (E) COUNTRY: USA
26           (F) ZIP: 27709
28       (v) COMPUTER READABLE FORM:
29           (A) MEDIUM TYPE: Floppy disk
30           (B) COMPUTER: IBM PC compatible
31           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
32           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
34      (vi) CURRENT APPLICATION DATA:
35           (A) APPLICATION NUMBER: US/10/016,236
36           (B) FILING DATE: 12-Dec-2001
37           (C) CLASSIFICATION:
77     (vii) PRIOR APPLICATION DATA:
40           (A) APPLICATION NUMBER: 08/996,685
41           (B) FILING DATE:
45           (A) APPLICATION NUMBER: US 08/761,543
46           (B) FILING DATE: 6-DEC-1996
49           (A) APPLICATION NUMBER: US 60/034,378
50           (B) FILING DATE: 27-DEC-1996
53           (A) APPLICATION NUMBER: US 60/034,379
54           (B) FILING DATE: 27-DEC-1996
57           (A) APPLICATION NUMBER: US 60/034,382
58           (B) FILING DATE: 27-DEC-1996
61           (A) APPLICATION NUMBER: US 60/034,730
62           (B) FILING DATE: 10-JAN-1997
65           (A) APPLICATION NUMBER: US 60/035,021
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C--> 35 and C--> 36 marked in left margin.

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 66              (B) FILING DATE: 10-JAN-1997
 69              (A) APPLICATION NUMBER: US 60/035,022
 70              (B) FILING DATE: 10-JAN-1997
 73              (A) APPLICATION NUMBER: US 60/035,024
 74              (B) FILING DATE: 10-JAN-1997
 78              (A) APPLICATION NUMBER: US 08/875,015
 79              (B) FILING DATE: 16-JUL-1997
 82    (viii) ATTORNEY/AGENT INFORMATION:
 83              (A) NAME: Meigs, J. Timothy
 84              (B) REGISTRATION NUMBER: 38,241
 85              (C) REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912
 87       (ix) TELECOMMUNICATION INFORMATION:
 88              (A) TELEPHONE: (919) 541-8587
 89              (B) TELEFAX: (919) 541-8689
 92 (2) INFORMATION FOR SEQ ID NO: 1:
 94       (i) SEQUENCE CHARACTERISTICS:
 95              (A) LENGTH: 5655 base pairs
 96              (B) TYPE: nucleic acid
 97              (C) STRANDEDNESS: single
 98              (D) TOPOLOGY: linear
100      (ii) MOLECULE TYPE: DNA (genomic)
102     (iii) HYPOTHETICAL: NO
104      (iv) ANTI-SENSE: NO
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110              (D) OTHER INFORMATION: /product= "1st exon of NIM1"
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114              (B) LOCATION: 3427..4162
115              (D) OTHER INFORMATION: /product= "2nd exon of NIM1"
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123              (A) NAME/KEY: exon
124              (B) LOCATION: 4586..4866
125              (D) OTHER INFORMATION: /product= "4th exon of NIM1"
127      (ix) FEATURE:
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129              (B) LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
132      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
134 TGTGATGCAA GTCATGGGAT ATTGCTTTGT GTTAAGTATA CAAAACCATC ACGTGGATAC        60
136 ATAGTCTTCA AACCAACCAC TAAACAGTAT CAGGTCATAC CAAAGCCAGA AGTGAAGGGT       120
138 TGGGATATGT CATTGGGTTT AGCGGTAATC GGATTGAACC CTTTCCGGTA TAAAATACAA       180
140 AGGCTTTCGC AGTCTCGGCG TATGTGTATG TCTCGGGGTA TCTACCATTT GAATCACAGA       240
142 ACTTTTATGT GCGAAGTTTT CGATTCTGAT TCGTTTACCT GGAAGAGATT AGAAAATTTG       300
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156  CTCTACAACA TAAACGCAGA GAAGTTGAAT TTAGTTTATG CAAAAAAAGA GGGATCTGAT    720
158  TGTTCTTTCG TTTGTTTTCC GTTTTGTTCT GATTACGAGA GGGTTGATCT GAACGGAAGA    780
160  AGCAACGGGC CGACACTTTA AAAAAAAAAT AAAAAAAATG GGCCGACAAA TGCAAACGTA    840
162  GTTGACAAGG ATCTCAAGTC TCAAGTCTCA ATTGGCTCGC TCATTGTGGG GCATAAATAT    900
164  ATCTAGTGAT GTTTAATTGT TTTTTATAAG GTAAAAGGA ATATTGAATT TTGTTTCTTA    960
166  GGTTTATGTA ATAATACCAA ACATTGTTTT ATGAATATTT AATCTGATTT TTTGGCTAGT   1020
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170  TGTCCCAATT TTCTCTCTTA AATAATATAT TAGTTAATAA AAGATATTTT AATATATTAG   1140
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190  TTCAACATAA TCTTACGTTG TTGTATTCAT AGGCATCTTT AACCTATCTT TTCATTTTCT   1740
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194  ATGCAGATTC CTTCTTCTTC TCAGTTTCCA GCAACATCGA GTCCGGAAAA CACCAATCAA   1860
196  GTGAAGGATG AGCCAAATTT GTTTAGACGT GTTATGAATT TGCTTTTACG TCGTAGTTAT   1920
198  TGAAAAAGCT GATTTATCGC ATGATTCAGA ACGAGAAGTT GAAGGCAAAT AACTAAAGAA   1980
200  GTCTTTTATA TGTATACAAT AATTGTTTTT AAATCAAATC CTAATTAAAA AAATATATTC   2040
202  ATTATGACTT TCATGTTTTT AATGTAATTT ATTCCTATAT CTATAATGAT TTTGTTGTGA   2100
204  AGAGCGTTTT CATTTGCTAT AGAACAAGGA GAATAGTTCC AGGAAATATT CGACTTGATT   2160
206  TAATTATAGT GTAAACATGC TGAACACTGA AAATTACTTT TTCAATAAAC GAAAAATATA   2220
208  ATATACATTA CAAAACTTAT GTGAATAAAG CATGAAACTT AATATACGTT CCCTTTATCA   2280
210  TTTTACTTCA AAGAAAATAA ACAGAAATGT AACTTTCACA TGTAAATCTA ATTCTTAAAT   2340
212  TTAAAAAATA ATATTTATAT ATTTATATGA AAATAACGAA CCGGATGAAA AATAAATTTT   2400
214  ATATATTTAT ATCATCTCCA AATCTAGTTT GGTTCAGGGG CTTACCGAAC CGGATTGAAC   2460
216  TTCTCATATA CAAAAATTAG CAACACAAAA TGTCTCCGGT ATAAATACTA ACATTTATAA   2520
218  CCCGAACCGG TTTAGCTTCC TGTTATATCT TTTTAAAAAA GATCTCTGAC AAAGATTCCT   2580
220  TTCCTGGAAA TTTACCGGTT TTGGTGAAAT GTAAACCGTG GGACGAGGAT GCTTCTTCAT   2640
222  ATCTCACCAC CACTCTCGTT GACTTGACTT GGCTCTGCTC GTCAATGGTT ATCTTCGATC   2700
224  TTTAACCAAA TCCAGTTGAT AAGGTCTCTT CGTTGATTAG CAGAGATCTC TTTAATTTGT   2760
226  GAATTTCAAT TCATCGGAAC CTGTTG ATG GAC ACC ACC ATT GAT GGA TTC GCC   2813
227                               Met Asp Thr Thr Ile Asp Gly Phe Ala
228                                ·1                  5
230  GAT TCT TAT GAA ATC AGC AGC ACT AGT TTC GTC GCT ACC GAT AAC ACC   2861
231  Asp Ser Tyr Glu Ile Ser Ser Thr Ser Phe Val Ala Thr Asp Asn Thr
232  10                  15                  20                  25
234  GAC TCC TCT ATT GTT TAT CTG GCC GCC GAA CAA GTA CTC ACC GGA CCT   2909
235  Asp Ser Ser Ile Val Tyr Leu Ala Ala Glu Gln Val Leu Thr Gly Pro
236                  30                  35                  40
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238 GAT GTA TCT GCT CTG CAA TTG CTC TCC AAC AGC TTC GAA TCC GTC TTT      2957
239 Asp Val Ser Ala Leu Gln Leu Leu Ser Asn Ser Phe Glu Ser Val Phe
240             45                  50                  55
242 GAC TCG CCG GAT GAT TTC TAC AGC GAC GCT AAG CTT GTT CTC TCC GAC      3005
243 Asp Ser Pro Asp Asp Phe Tyr Ser Asp Ala Lys Leu Val Leu Ser Asp
244             60                  65                  70
246 GGC CGG GAA GTT TCT TTC CAC CGG TGC GTT TTG TCA GCG AGA AGC TCT      3053
247 Gly Arg Glu Val Ser Phe His Arg Cys Val Leu Ser Ala Arg Ser Ser
248        75                  80                  85
250 TTC TTC AAG AGC GCT TTA GCC GCC GCT AAG AAG GAG AAA GAC TCC AAC      3101
251 Phe Phe Lys Ser Ala Leu Ala Ala Ala Lys Lys Glu Lys Asp Ser Asn
252 90                  95                  100                 105
254 AAC ACC GCC GCC GTG AAG CTC GAG CTT AAG GAG ATT GCC AAG GAT TAC      3149
255 Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu Ile Ala Lys Asp Tyr
256             110                 115                 120
258 GAA GTC GGT TTC GAT TCG GTT GTG ACT GTT TTG GCT TAT GTT TAC AGC      3197
259 Glu Val Gly Phe Asp Ser Val Val Thr Val Leu Ala Tyr Val Tyr Ser
260             125                 130                 135
262 AGC AGA GTG AGA CCG CCG CCT AAA GGA GTT TCT GAA TGC GCA GAC GAG      3245
263 Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser Glu Cys Ala Asp Glu
264             140                 145                 150
266 AAT TGC TGC CAC GTG GCT TGC CGG CCG GCG GTG GAT TTC ATG TTG GAG      3293
267 Asn Cys Cys His Val Ala Cys Arg Pro Ala Val Asp Phe Met Leu Glu
268        155                 160                 165
270 GTT CTC TAT TTG GCT TTC ATC TTC AAG ATC CCT GAA TTA ATT ACT CTC      3341
271 Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro Glu Leu Ile Thr Leu
272 170                 175                 180                 185
274 TAT CAG GTAAAACACC ATCTGCATTA AGCTATGGTT ACACATTCAT GAATATGTTC      3397
275 Tyr Gln
278 TTACTTGAGT ACTTGTATTT GTATTTCAG AGG CAC TTA TTG GAC GTT GTA GAC     3450
279                                     Arg His Leu Leu Asp Val Val Asp
280                                         190                 195
282 AAA GTT GTT ATA GAG GAC ACA TTG GTT ATA CTC AAG CTT GCT AAT ATA      3498
283 Lys Val Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu Ala Asn Ile
284             200                 205                 210
286 TGT GGT AAA GCT TGT ATG AAG CTA TTG GAT AGA TGT AAA GAG ATT ATT      3546
287 Cys Gly Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile
288             215                 220                 225
290 GTC AAG TCT AAT GTA GAT ATG GTT AGT CTT GAA AAG TCA TTG CCG GAA      3594
291 Val Lys Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser Leu Pro Glu
292             230                 235                 240
294 GAG CTT GTT AAA GAG ATA ATT GAT AGA CGT AAA GAG CTT GGT TTG GAG      3642
295 Glu Leu Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu Gly Leu Glu
296        245                 250                 255
298 GTA CCT AAA GTA AAG AAA CAT GTC TCG AAT GTA CAT AAG GCA CTT GAC      3690
299 Val Pro Lys Val Lys Lys His Val Ser Asn Val His Lys Ala Leu Asp
300 260                 265                 270                 275
302 TCG GAT GAT ATT GAG TTA GTC AAG TTG CTT TTG AAA GAG GAT CAC ACC      3738
303 Ser Asp Asp Ile Glu Leu Val Lys Leu Leu Leu Lys Glu Asp His Thr
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304                    280                    285                    290
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307 Asn Leu Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala Tyr Cys Asn
308             295                    300                    305
310 GTG AAG ACC GCA ACA GAT CTT TTA AAA CTT GAT CTT GCC GAT GTC AAC      3834
311 Val Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala Asp Val Asn
312             310                    315                    320
314 CAT AGG AAT CCG AGG GGA TAT ACG GTG CTT CAT GTT GCT GCG ATG CGG      3882
315 His Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala Ala Met Arg
316       325                    330                    335
318 AAG GAG CCA CAA TTG ATA CTA TCT CTA TTG GAA AAA GGT GCA AGT GCA      3930
319 Lys Glu Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly Ala Ser Ala
320 340                    345                    350                    355
322 TCA GAA GCA ACT TTG GAA GGT AGA ACC GCA CTC ATG ATC GCA AAA CAA      3978
323 Ser Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile Ala Lys Gln
324             360                    365                    370
326 GCC ACT ATG GCG GTT GAA TGT AAT AAT ATC CCG GAG CAA TGC AAG CAT      4026
327 Ala Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Gln Cys Lys His
328             375                    380                    385
330 TCT CTC AAA GGC CGA CTA TGT GTA GAA ATA CTA GAG CAA GAA GAC AAA      4074
331 Ser Leu Lys Gly Arg Leu Cys Val Glu Ile Leu Glu Gln Glu Asp Lys
332             390                    395                    400
334 CGA GAA CAA ATT CCT AGA GAT GTT CCT CCC TCT TTT GCA GTG GCG GCC      4122
335 Arg Glu Gln Ile Pro Arg Asp Val Pro Pro Ser Phe Ala Val Ala Ala
336       405                    410                    415
338 GAT GAA TTG AAG ATG ACG CTG CTC GAT CTT GAA AAT AGA G              4162
339 Asp Glu Leu Lys Met Thr Leu Leu Asp Leu Glu Asn Arg
340 420                    425                    430
342 GTATCTATCA AGTCTTATTT CTTATATGTT TGAATTAAAT TTATGTCCTC TCTATTAGGA   4222
344 AACTGAGTGA ACTAATGATA ACTATTCTTT GTGTCGTCCA CTGTTTAG  TT GCA CTT     4278
345                                                       Val Ala Leu
346                                                               435
348 GCT CAA CGT CTT TTT CCA ACG GAA GCA CAA GCT GCA ATG GAG ATC GCC      4326
349 Ala Gln Arg Leu Phe Pro Thr Glu Ala Gln Ala Ala Met Glu Ile Ala
350             440                    445                    450
352 GAA ATG AAG GGA ACA TGT GAG TTC ATA GTG ACT AGC CTC GAG CCT GAC      4374
353 Glu Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu Glu Pro Asp
354             455                    460                    465
356 CGT CTC ACT GGT ACG AAG AGA ACA TCA CCG GGT GTA AAG ATA GCA CCT      4422
357 Arg Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys Ile Ala Pro
358             470                    475                    480
360 TTC AGA ATC CTA GAA GAG CAT CAA AGT AGA CTA AAA GCG CTT TCT AAA      4470
361 Phe Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala Leu Ser Lys
362       485                    490                    495
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365 Thr
366 500
368 TAAATGATCT TTAAACATGG TTTTGTTACT TGCTGTCTGA CCTTGTTTTT TTTATCATCA    4584
370 G  TG GAA CTC GGG AAA CGA TTC TTC CCG CGC TGT TCG GCA GTG CTC       4629
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/27/2002
PATENT APPLICATION: US/10/016,236   TIME: 10:39:23

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Output Set: N:\CRF3\03272002\J016236.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:18; Xaa Pos.29,34

VERIFICATION SUMMARY   DATE: 03/27/2002
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Input Set : N:\Crf3\RULE60\10016236.raw
Output Set: N:\CRF3\03272002\J016236.raw

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L:36 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:555 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=3
L:631 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=4
L:707 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=5
L:1417 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:2159 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=17
L:2183 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=18
L:2195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:16
L:2198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:32
L:2207 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=19
L:2231 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=20
L:2252 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=21
L:2276 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=22
L:2297 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=23
L:2321 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=24
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